

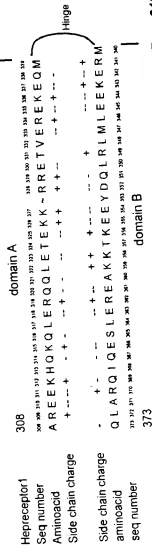
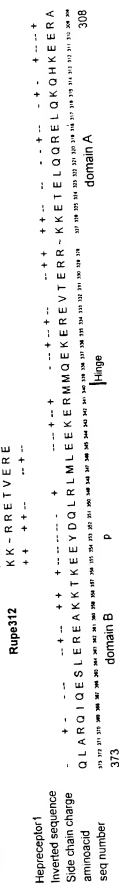
FIGURE 1

Primary/secondary structure of the Heptareceptor

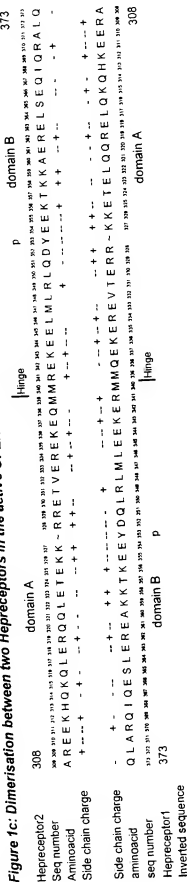
Note how the highly charged region matches positive to negative charges when either binding to itself, to a synthetic ligand such as Rupe312, or bim

— = continuity of amino acid sequence
p = phosphate group on tyrosine

FIGURE 4c: Inactive FOLDED conformation of the Heparceptor

373 **3.1.1. Activation of the Hsp90 receptor binding a ligand (Rupe312)**

3.1.3. *Representors in the active OPEN conformation*



Cellular locations and complexes of ezrin

